OIPE

RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/10/024,632   TIME: 17:46:56

Input Set : **N:\paola\10024632.txt**
Output Set: **N:\CRF3\01152002\J024632.raw**

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 3 <110> APPLICANT: Monsanto Technology LLC
 4        He, Steve S.
 5        Dotson, Stanton B.
 7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ASSOCIATED WITH PLANT CELL
PROLIFERATION AND
 8        GROWTH AND USES THEREOF
10 <130> FILE REFERENCE: 38-21(51837)B
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C--> 12 **<140> CURRENT APPLICATION NUMBER: US/10/024,632**
C--> 12 **<141> CURRENT FILING DATE: 2001-12-19**
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13 <151> PRIOR FILING DATE: 2000-12-21
15 <160> NUMBER OF SEQ ID NOS: 33
17 <170> SOFTWARE: PatentIn version 3.1
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21 <212> TYPE: DNA
22 <213> ORGANISM: Glycine max
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35 gcagagatta acatgatgat tagtttattt gccaagcaat gccttccttc gtgagatata     180
37 aactgctagc aatttcaaat cttttcgagt aaccaaaaag aaaaaaacaa aaagcaagaa     240
39 g atg aag cgc ata aat gag agt aac aac acc gat gat gga aac aat cat     289
40   Met Lys Arg Ile Asn Glu Ser Asn Asn Thr Asp Asp Gly Asn Asn His
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43 aac tgg ttg ggg ttc tct ctc tca ccc cac atg aaa atg gag gct act     337
44 Asn Trp Leu Gly Phe Ser Leu Ser Pro His Met Lys Met Glu Ala Thr
45             20                  25                  30
47 tca gca gcc act gtt ccg aca acc ttc tac atg tcc cct tct caa tct     385
48 Ser Ala Ala Thr Val Pro Thr Thr Phe Tyr Met Ser Pro Ser Gln Ser
49             35                  40                  45
51 cac ttg tcc aac ttc gga atg tgt tac ggt gtc gga gaa aat ggt aac     433
52 His Leu Ser Asn Phe Gly Met Cys Tyr Gly Val Gly Glu Asn Gly Asn
53       50                  55                  60
55 ttc cat tct cca ctt acg gtt atg cct ctc aag tct gat ggg tca ctt     481
56 Phe His Ser Pro Leu Thr Val Met Pro Leu Lys Ser Asp Gly Ser Leu
57 65                  70                  75                  80
59 tgt atc ttg gaa gct ctc aaa aga tca caa acg caa gtg atg gtg cca     529
60 Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
61             85                  90                  95
63 act tcg tct ccg aaa ttg gag gac ttt cta ggt ggt gca act atg gga     577
64 Thr Ser Ser Pro Lys Leu Glu Asp Phe Leu Gly Gly Ala Thr Met Gly
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67 act cac gaa tat gga agc cac gag aga ggt ttg agc cta gac agc atc     625
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72 Tyr Tyr Asn Ser Gln Asn Ala Glu Ala Gln Pro Asn Arg Asp Leu Leu
73     130             135             140
75 tca caa ccc ttc agg caa caa ggt cat atg agt gtc caa aca cac cct      721
76 Ser Gln Pro Phe Arg Gln Gln Gly His Met Ser Val Gln Thr His Pro
77 145             150             155                 160
79 tat tac tca ggc ctt gct tgc cat ggt tta tat caa gca ccg ttg gag      769
80 Tyr Tyr Ser Gly Leu Ala Cys His Gly Leu Tyr Gln Ala Pro Leu Glu
81             165             170             175
83 gaa gaa aca aca aag gaa acg cac gtg tcg gat tgc agc tcc cta atg      817
84 Glu Glu Thr Thr Lys Glu Thr His Val Ser Asp Cys Ser Ser Leu Met
85         180             185             190
87 cct caa atg aca gaa ggc ttg aaa aac tgg gtg gct cca aca agg gag      865
88 Pro Gln Met Thr Glu Gly Leu Lys Asn Trp Val Ala Pro Thr Arg Glu
89         195             200             205
91 ttt tca act cac cag cag gtt ttg gag cag caa atg aat tgt ggc atg      913
92 Phe Ser Thr His Gln Gln Val Leu Glu Gln Gln Met Asn Cys Gly Met
93     210             215             220
95 ggg aat gag aga aat ggt gtg tct tta gga tct gtg ggg tgt gga gag      961
96 Gly Asn Glu Arg Asn Gly Val Ser Leu Gly Ser Val Gly Cys Gly Glu
97 225             230             235             240
99 tta cag tct cta agc tta tct atg agt cct ggt tct cag tct agt tgt     1009
100 Leu Gln Ser Leu Ser Leu Ser Met Ser Pro Gly Ser Gln Ser Ser Cys
101             245             250             255
103 gtc act gct cct tct gga aca gat tct gtt gct gtg gat gca aag aag     1057
104 Val Thr Ala Pro Ser Gly Thr Asp Ser Val Ala Val Asp Ala Lys Lys
105             260             265             270
107 aga ggg cat gct aaa ctt ggt cag aag cag cct gtg cat aga aaa tct     1105
108 Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys Ser
109         275             280             285
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119 aag aag gaa ggg caa act agg aaa gga cga caa gtg tat ttg ggg ggt     1249
120 Lys Lys Glu Gly Gln Thr Arg Lys Gly Arg Gln Val Tyr Leu Gly Gly
121             325             330             335
123 tat gat atg gag gag aaa gct gca aga gcc tat gat ctc gcg gcc ctt     1297
124 Tyr Asp Met Glu Glu Lys Ala Ala Arg Ala Tyr Asp Leu Ala Ala Leu
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127 aag tac tgg gga cct tca acg cat ata aac ttt tcg ata gag aat tac     1345
128 Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr
129         355             360             365
131 caa gtt caa ctt gag gaa atg aag aac atg agc aga cag gaa tac gtt     1393
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137 385                    390                    395                    400
139 tac aga ggg gtc aca agg cat cac caa cat gga aga tgg caa gcg agg      1489
140 Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
141                        405                    410                    415
143 ata ggc aga gtt gct ggg aac aaa gac ctt tac ctt ggg acg ttc agc      1537
144 Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
145                        420                    425                    430
147 acc caa gag gaa gca gca gaa gca tac gat gta gcg gcg atc aaa ttt      1585
148 Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe
149            435                    440                    445
151 cgc ggc gca aat gca gtc aca aac ttt gac att tca aga tac gat gtg      1633
152 Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
153        450                    455                    460
155 gag aga atc atg gcc agt agc aat ctc ctc gct ggg gag ctt gca agg      1681
156 Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg
157 465                    470                    475                    480
159 cgt aag aaa gat aac gat cct aga aac aag gac ata gac tac aac aag      1729
160 Arg Lys Lys Asp Asn Asp Pro Arg Asn Lys Asp Ile Asp Tyr Asn Lys
161                        485                    490                    495
163 agt gta gta aca agt gtg aac aat gag gaa acg gtt caa gtt caa gca      1777
164 Ser Val Val Thr Ser Val Asn Asn Glu Glu Thr Val Gln Val Gln Ala
165                        500                    505                    510
167 gga aac aac aat aat gaa aac gac tca gag tgg aag atg gtt tta ttt      1825
168 Gly Asn Asn Asn Asn Glu Asn Asp Ser Glu Trp Lys Met Val Leu Phe
169            515                    520                    525
171 aac cac cct tca cag cag caa cag gca aat ggc aat ggc agt gac caa      1873
172 Asn His Pro Ser Gln Gln Gln Gln Ala Asn Gly Asn Gly Ser Asp Gln
173        530                    535                    540
175 aaa ata atg aac tgt gga aat tac aga aac agt gca ttt tct atg gcc      1921
176 Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala
177 545                    550                    555                    560
179 cta caa gat ctt att ggg att gat tcg gtg ggt tct ggg cag cat aat      1969
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188 Ser Leu Val Thr Ser Leu Ser Ser Ser Arg Glu Ala Ser Pro Glu Lys
189            595                    600                    605
191 agg ggt ccc tcg ctt ctg ttc cca atg cct cca atg gaa aca aag att      2113
192 Arg Gly Pro Ser Leu Leu Phe Pro Met Pro Pro Met Glu Thr Lys Ile
193        610                    615                    620
195 gtg aac ccc att ggt acc agt gtt acc tct tgg cta ccc tca cca acg      2161
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236 65                  70                  75                  80
239 Cys Ile Leu Glu Ala Leu Lys Arg Ser Gln Thr Gln Val Met Val Pro
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264             180                 185                 190
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268         195                 200                 205
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280             245                 250                 255
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284             260                 265                 270
287 Arg Gly His Ala Lys Leu Gly Gln Lys Gln Pro Val His Arg Lys Ser
288         275                 280                 285
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304             340             345             350
307 Lys Tyr Trp Gly Pro Ser Thr His Ile Asn Phe Ser Ile Glu Asn Tyr
308             355             360             365
311 Gln Val Gln Leu Glu Glu Met Lys Asn Met Ser Arg Gln Glu Tyr Val
312     370             375             380
315 Ala His Leu Arg Arg Lys Ser Ser Gly Phe Ser Arg Gly Ala Ser Ile
316 385             390             395             400
319 Tyr Arg Gly Val Thr Arg His His Gln His Gly Arg Trp Gln Ala Arg
320             405             410             415
323 Ile Gly Arg Val Ala Gly Asn Lys Asp Leu Tyr Leu Gly Thr Phe Ser
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327 Thr Gln Glu Glu Ala Ala Glu Ala Tyr Asp Val Ala Ala Ile Lys Phe
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331 Arg Gly Ala Asn Ala Val Thr Asn Phe Asp Ile Ser Arg Tyr Asp Val
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335 Glu Arg Ile Met Ala Ser Ser Asn Leu Leu Ala Gly Glu Leu Ala Arg
336 465             470             475             480
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344             500             505             510
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348             515             520             525
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352     530             535             540
355 Lys Ile Met Asn Cys Gly Asn Tyr Arg Asn Ser Ala Phe Ser Met Ala
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360             565             570             575
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VERIFICATION SUMMARY   DATE: 01/15/2002
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L:12   M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:2180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
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